

Appendix A

Clustal V alignment of the amino acid sequences having SEQ ID NOs:2, 4, and 6 in the instant application with the cobalamin independent methionine synthases from *E. coli* (NCBI gi No. 836660), *Catharanthus roseus* (NCBI gi No. 1362086), *Coleus blumei* (amino acids 21-84, NCBI gi No. 974782), *Arabidopsis thaliana* (NCBI gi No. 2738248), *Mesembryanthemum crystallinum* (NCBI gi No. 1814403), *Arabidopsis thaliana* (NCBI gi No), and *Solanum tuberosum* (NCBI gi No. 8339545). Amino acids conserved among all the sequences are indicated by an asterisk (*) below the alignment and those conserved only among the plant sequences are indicated by a plus sign (+). The conserved domain containing the active site cysteine (corresponding to *E. coli* 726) is shown boxed.

	1	60
836660	MTILNHTLGFPRVGLRRELKKAQESYWAGNSTREELLAVGRELRARHWDQKQAGIDLLP	
1362086	MA--SHIVGYPRMGPKRELKFALESFWDKKSSAEDLQKVAADLRSSIWKQMADAGIKYIP	
SEQIDNO02	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKVATDLRSSIWKQMSEAGIKYIP	
SEQIDNO04	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLQKVAADLRSSIWKQMAGAGIKYIP	
SEQIDNO6	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLKKVAADLRSSIWKQMADAGIKYIP	
8439545	MA--SHVVGYPYPRMGPKRELKFALESFWDGKSSAEDLKKVSADLRSSIWKQMSDAGIKYIP	
CAA89019	MA--SHIVGYPRMGPKRELKFALESFWDGKSSAEDLEKQCQLILGIHL-KQMSDAGIKYIP	
AAB41896	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLKKVSADLRSSIWKQMADAGIKYIP	
2738248	MA--SHIVGYPRMGPKRELKFALESFWDGKSTAEDLQKVSADLRSSIWKQMSAAGTKFIP	
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	61	120
836660	VGDFAWYDHVLTTSLLLGNVPARHQNKDGSVDIDTLFRIGRGRAPTGEPAAAAEMTKWFN	
1362086	SNTFSYYDQVLDTTAMLGAVPPRYNFAGGEIGFDITYFSMARGNASV----PAMEMTKWFD	
SEQIDNO02	SNTSSYYDQVLDTTAMLGAVPERYSWTGGEIGLSTYFSMARGNATV----PAMEMTKWFD	
SEQIDNO04	SNTFSFYDQLLDATATLGAVPPRYGWTGGEIGFDITYFSMARGNATV----PAMEMTKWFD	
SEQIDNO6	SNTFSYYDQVLDTTAMLGAVPARYNWAGGEIAFDITYFSMARGNASV----PAMEMTKWFD	
8439545	SNTFSYYDQVLDTTAMLGAVPSRYNWTGGEIEFGTYFSMARGNASV----PAMEMTKWFD	
CAA89019	SNTFSYYDQVLDTTAMLGAVPPRYNWTGGEIGFSTYFSMARGNASV----PAMEMTKWFD	
AAB41896	SNTFSYYDQVLDTTAMLGAVPPRYGWTGGEIEFDVYFSMARGNASV----PAMEMTKWFD	
2738248	SNTFAHYDQVLDTTAMLGAVPPRYGYTGGEIGLDVYFSMARGNASV----PAMEMTKWFD	
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	121	180
836660	TNYHYMVPEFVKQQQFKLTWTQLLDEVDEALALGHKVKPVLLGPVTWLWLKG-VKGEQ--	
1362086	TNYHYIVPELGPEVNFSYASHKAVNEYKEAKELGVDTPVPLVGPVTFLLLSKPAKGVEKT	
SEQIDNO02	TNYHFIVPELGPSTKFTYASHKAVSEYKEAKALGIDTVPVLVGPVSYLLLSKPAKGVEKS	
SEQIDNO04	TNYHFIVPELGPDVNFTXASQKAVDEYKEAKALGVDTPVPLVGPVSYLLLSKPAKGVEKS	
SEQIDNO6	TNYHFIVPELGPDVNFSYASHKAVDEYKEAKGLGVDTPVPLIGPVSYLLLSKPAKGVEKS	
8439545	TNYHFIVPELGPDVNFSYASHKAVNEYKEAKAQGVDTVPVLVGPVSYLLLSKPAKGVEKS	
CAA89019	TNYHFIVPELGPDKFSYASHKAVNEYKEAKALGVDTPVPLVGPVSYLILSKPAKGVEKT	
AAB41896	TNYHFIVPELGPPEVNFSYASHKAVLEYKEAKALGVDTPVPLVGPVSYLLLSKQAKGVDKS	
2738248	TNYHYIVPELGPPEVNFSYASHKAVNEYKEAKALGVDTPVPLVGPVSYLLLSKAAGVDKS	
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181 240

836660 FDRLSLLNDILPVYQQVLAELAKRGIEWQIDEPALVLELPQAWLDAYKPAYDALQGGV -

1362086 FPLLSLLDKILPVYKEVIGELKAAGASWQFDEPTLVLDLESHQLEAFTKAYSELESTLS

SEQIDNO02 FSLLSLLGSILPIYKEVVAELKAAGASWQFDEPTLVKDLDAHELAASFSSAYAELESSFS

SEQIDNO04 FSLLSLLPKVLAVYKEVIAELKAAGASWQFDEPTLVLDLESHKLQAFDAYAELEAPALS

SEQIDNO6 FPLLSLLDKVLPYKEVIAELKAAGASWQFDEPTLVLDLQAHQLEAFTKAYAELESSLS

8439545 FPLLSLLDKILPIYKEVIAELKAAGASWQFDEPTLVLDLESHKLEAFTKAYADLESSLS

CAA89019 FPLLSLLDKILPIYKEVIAELKAAGASWQFDEPTLVLDLESHQLDAFTKAYAELESSLS

AAB41896 FDLLSLLPKILPIYKEVVAELKEAGASWQFDEPLLVMDLESHKLQAFSAAYADLESTLS

2738248 FELLSSLLPKILPIYKEVITELKAAGATWQFDEPLVMDLEGQKLQAFGTAYAELESTLS

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241 300

836660 --KLTLTYFEGVTPN-LDTITALP-VQGLHVDLVHKGDDVAELHKRLPSDWLLSAGLIN

1362086 GLNVIVETTYFADIPAETIKILTALKGVTGFGFDLVRGAKTLDLTKGGFPPSGKYLFAGVVD

SEQIDNO02 GLNVLIETTYFADIPAESYKTLTSLSGVTAYGFDLIRGAKTLDLIRSSFPSGKYLFAGVVD

SEQIDNO04 DLNVIVETTYFADIPAETIKILTALKGVTGFGFDLVRGTHTLTLTKGGFPPSGKYLFAGVVD

SEQIDNO6 GLNVLTETTYFADVPAAFKTLTALKGVTAFGFDLVRGAQTLDLTKGGFPPSGKYLFAGVVD

8439545 GLNVIVETTYFADVPAAFKTLTALKGVTAFGFDLVRGTQTLELIKSSFPSGKYLFAGVVD

CAA89019 GLSTLIETTYFADVPAPAYKTLTSLSGISGFGFDLVRGAQTIELIKGGFPPSGKYLFAGVVD

AAB41896 GLNVVVETTYFADVTAEAYKTLTSLKGVTGFGFDLVRGTKTLDLVKAEPFSGKYLFAGVVD

2738248 GLNVIVETTYFADIPAETIKILTALKGVTAFGFDLVRGTKTLDLVKAGFPEGKYLFAGVVD

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301 360

836660 GRNVWRADLTEKYAQIKD---IVGKRDWLWASSCSLLHSPIDLSVETRLDAEVKSWFAFA

1362086 GRNIWANDLAASLSTLQSLEGIVGKDKLVVSTSCSLHHTAVDLVNEPKLDKEIKSWLAFA

SEQIDNO02 GRNIWADDLAASLSTLHSLAVAGKDKLVVSTSCSLMHTAVDLVNETKLDDEIKSWLAFA

SEQIDNO04 GRNIWANDLAASLTTLQGLEIGVGDVSTSSSLHHTAVDLVNETKLDDEIKSWLAFA

SEQIDNO6 GRNIWANDLAASLNLQSLQLEGIVGKDKLVVSTSCSLHHTAVDLVNETKLDDEIKSWLAFA

8439545 GRNIWANDLAASLALLQSLQLEGVVGKDKLVASTSCSLHHTAVDLINETKLDDEIKSWLAFA

CAA89019 GRNIWANDLASSITTLQALEGIVGKDKLVVSTSSSLHHTAVDLVNEPKLDQEIKSWLAFA

AAB41896 GRNIWANDLAASLATLEALEGIVGKDKLVVSTSCSLHHTAVDLINETKLDDEIKSWLAFA

2738248 GRNIWANDFAASLSTLQALEGIVGKDKLVVSTSCSLHHTAVDLINETKLDDEIKSWLAFA

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361 420

836660 LQKCHELALLRDALNSGDTAAL-AEWSAPIQARRHSTRVHNPAVEKRLAAITAQDSQRAN

1362086 AQKVVEVNALAKALAGEKDEAFFSENAAAQASRKSSPRVTNQAVQKAAAALRGSDHRRAT

SEQIDNO02 AQKVVEVNALAKALAGQKDEVYFAANAAAQASRRSSPRVTNEEVQKAAAALRGSDHRRST

SEQIDNO04 AQKIVEVNALAKALSGNKDVAFSANAAAQASRKSSPRVTNEAVQKAAAALRGSDHRRAT

SEQIDNO6 AQKVVEVNALAKALAGHKDEAFFSANATAQASRKSSPRVTNEAVQKAAAALRGSDHRRAT

8439545 AQKVVEVNALAKALSGAKDEAFFSANAAAQASRKSSPRVTNEAVQKASAAALRGSDHRRAT

CAA89019 AQKIVEVNALAKALTGHKDEAFFSPNAAAQASRKSSPRVTNEAVQKAAAALRGSEHRRVT

AAB41896 AQKVLEVNALAKALSGQKDEAFFSANAAAASRKSSPRVTNEAVQKAATALRGSDHRRAT

2738248 AQKVVEVNALAKALAGQKDEALFSANAAAASRRSSPRVTNEGVQKAAAALRGSDHRRAT

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	421		480
836660	VYEVRAEAQRARFKLPAPWPTTTIGSFQPQTTEIRTLRLDFKKGNLDANNYRTGIAEHKQA		
1362086	TVSARLDAQQKKLNLPLVLPPTTTIGSFQPTLELRRVRREYKAKKISEDYVKAKEEISKV		
SEQIDN002	TVSARLDAQQKKLNLPLVLPPTTTIGSFQPTVELRRVRREYKAKKITEDEYISAIKEEISKV		
SEQIDN004	NVSARLDAQQKKLNLPLPPTTTIGSFQPTVELRRVRREFKANKISEEEYVKSIIKEEIRKV		
SEQIDN06	NVSSRLDAQQKKLNLPLVLPPTTTIGSFQPTVELRRVRREYKAKKISEEEYVKAIAEIKKV		
8439545	NVSARLDAQQKKLNLPLPPTTTIGSFQPTVELRRVRREYKAKKISEEEYVKAITEEIKKV		
CAA89019	NVSARLDAQQKKLNLPLPPTTTIGSFQPTVELRRVRREFKPTRISEEEYVKAIEEINKV		
AB41896	TVSSRLDAQQKKLNLPLPPTTTIGSFQPTVELRRVRREYKAKKISEEEYVKAIEEISKV		
2738248	NVSARLDAQQKKLNLPLPPTTTIGSFQPTVELRRVRREYKAKKVSEEDYVKAIEEIKKV		
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	481	540
836660	IVEQERLGLDVLVHGEAERNDMVEYFGEHLDFGVFTQNGWVQSYGSRVCVKPPIVIGDISR	
1362086	VKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
SEQIDNO02	VKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
SEQIDNO04	VELQEELDDIDVLVHGEPERNDMVEYFGEQLSGFAFTVNGWVQSYGSRVCVKPPIIYGDVSR	
SEQIDNO6	VDLQEELDDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
8439545	VDLQEELDDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
CAA89019	VKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
AAB41896	VKLQEELDIDVLVHGEPERNDMVEYFGEQLSGFAFSANGWVQSYGSRVCVKPPIIYGDVSR	
2738248	VDLQEELDDIDVLVHGEPERNDMVEYFGEQLSGFAFTANGWVQSYGSRVCVKPPIIYGDVSR	
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	541	600
836660	PAPITVEWAKYAQSLTDKPVKGMLTGPVTILCWSFPREDVSRETI AK QIALALRDEVDL	
1362086	PNPMTVFWSQTAAQSMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
SEQIDNO02	PNPMTVFWSKMAQSMTPRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKKEVEDL	
SEQIDNO04	PKPMTVFWSSLAQSFTKRPMKGMLTGPVTILNWSFVRNDQPRSETTYQIALAIKDEVEDL	
SEQIDNO6	PNPMTVFWSKTAQSMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
8439545	PKPMTVFWSSKAQEMTKRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
CAA89019	PKPMTVFWSTAAQSMTQRPMKGMLTGPVTILNWSFVRNDQPRFETCYQIALAIKDEVEDL	
AAB41896	PNPMTVFWSSMAQSMTARPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKNEVEDL	
2738248	PKAMTVFWSAMAQSMTSRPMKGMLTGPVTILNWSFVRNDQPRHETCYQIALAIKDEVEDL	
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	601		660
836660	EAAGIGIIQIDEPALRQGLPLRRSDWDAYLQWGVEAFRINAATAVAKDDTQIHTHMCYCEFN		
1362086	EKAGINVIQIDEAALREGLPLRKAEHAFYLDWAVHSFRITNLPLODTTQIHTHMCYSNFN		
SEQIDNO02	EAAGIQVIQIDEAALREGLPLRKSEHAFYLDWAVHSFRITNCGVQDTTQIHTHMCYSNFN		
SEQIDNO04	EKAGITVIQIDEAALREGLPLRKSEQAHYLDWAVHAFRITNVGVQDTTQIHTHMCYSNFN		
SEQIDNO6	EKAGITVIQIDEAALREGLPLRKAEHAFYLNWAVHSFRITNVGIQDTTQIHTHMCYSNFN		
8439545	EKAGITVIQIDEAALREGLPLRKAEHAFYLNWAVHSFRITNVGIEDTTQIHTHMCYSNFN		
CAA89019	EKAGITVIQIDEAALREGLPLRKSEHAFYLDWAVHSFRITNVGVQDTTQIHTHMCYSNFN		
AAB41896	EKAGINVIQIDEAALREGLPLRKSEHDFYLKWAVHSFRITNVGVQDTTQIHTHMCYSNFN		
2738248	EKGIGIVIQIDEAALREGLPLRKSEHAFYLDWAVHSFRITNCGVQDSTQIHTHMCYSNFN		
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[illegible]

	721		771
836660	LKKAAKRIPAER	LWVNPDCGLKTR	GWPETRAALANMVQAAQNLRRG-----
1362086	INKMLAVLDTNI	LWVNPDCGLKTR	KYAEVKPALENMVSAAKLIRTQLASAK
SEQIDNO02	VEKMLAVFDTNI	LWVNPDCGLKTR	KYTEVKPALTNMVSATKLIRTQLASAK
SEQIDNO04	INKMLAVLEKNI	LWVNPDCGLKTR	KYTEVKPPSQNMVAAAKLIRYELA--K
SEQIDNO6	VNKMLAVLDTNI	LWVNPDCGLKTR	KYAEVKPALENMVSAAKAIRTQLASSK
8439545	VNKMLAVLDTNI	LWVNPDCGLKTR	KYTEVKPALQNMVSAAKTIRTQLASAK
CAA89019	INKMLAVLETNI	LWVNPDCGLKTR	KYAEVKPALENMVAAAKLLRTQLASAK
AAB41896	IRKMLAVLESNV	LWVNPDCGLKTR	KYGEVNPALSNMVAAAKQLRQELASAK
2738248	VNKMLAVLEQNI	LWVNPDCGLKTR	KYTEVKPALKNMVDAAKLIRSQLASAK
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